AMENDMENTS TO THE CLAIMS:

1-10. (Canceled)

11. (Presently Amended) ~~**Method according to**~~ **The method of** claim ~~**6**~~ **19**, characterised in that the universal primers are selected from the group consisting of:

5'TCCGGCATGTGCAAGGCCGG3' (SEQ ID NO: 1),

5'CTCCATGTCGTCCCAGTTGG3' (SEQ ID NO: 2),

5'ACCAACTGGGACGACATGGAGAAGATCTGGC3' (SEQ ID NO: 3),

5'TACATGGCNGGGGTGTTAAAGGTCTCAAAC3' (SEQ ID NO: 4),

5'TGCCCTGAGGCCCTCTTCCAGCCTTCCTTC3' (SEQ ID NO: 5),

5'GGGTACATGGTGGTGCCGCCAGACAGCACNGTGTTGGC3' (SEQ ID NO: 6),

5'GCCAACACNGTGCTGTCTGGCGGCACCACCATGTACCC3' (SEQ ID NO: 7) and

5'TCGTACTCCTGCTTGCTGATCCACATCTG3' (SEQ ID NO: 8).

12. (Canceled)

13. (Presently Amended) ~~**Method according to**~~ **The method of** claim ~~**2**~~ **16**, characterised in that the ~~**samples are**~~ **sample is** taken from horse, goat, rabbit, dog, cat, chimpanzee, human and/or brown bear tissue.

14 -15. (Canceled)

16. (New) A method for genetic identification of biological species using a sample of biological material derived from a single species or from a heterogeneous mixture of species and/or subspecies, characterised in that it comprises:

(a) DNA extraction from the sample;

(b) amplification of one or more regions of the DNA of the sample, said one or more regions selected from the group consisting of a region corresponding to the region between positions 1130 and 1473 of the human cytoplasmic beta-actin gene, a region corresponding to the region between positions 1452 and 2063 of the human cytoplasmic beta-actin gene, a region corresponding to the region between positions 2438 and 2680 of the human cytoplasmic beta-actin gene, and a region corresponding to the region between positions 2642 and 2960 of the human cytoplasmic beta-actin gene, said position numbers being relative to SEQ ID NO:9 which comprises the full DNA sequence of the human locus HUMACCYBB Accession number M10277, verison M10277.1, GI:177967;

(c) analysis of the one or more amplified regions to determine the size in base-pairs and/or the precise DNA sequence thereof; and

(d) taxonomic identification of the biological species or subspecies from which the sample was derived by comparison of the size and/or DNA sequence characteristics of said one or more regions with a database containing pre-established size and/or DNA sequence characteristics of the corresponding regions of the cytoplasmic beta-actin gene of a plurality of species and/or subspecies.

17. (New) The method of claim 16, characterised in that in the amplification step gene segments of evolutionary divergent regions of the cytoplasmic beta-actin gene are amplified using DNA oligonucleotide primers having evolutionary DNA sequence conservation greater than 98% between species and subspecies.

18. (New) The method of claim 16, characterised in that in the amplification step the segments to be amplified comprise the whole intronic DNA sequence and at least a portion of the flanking exonic sequences, for each of the B, C, D and E introns as annotated in the GenBank Record of the human locus HUMACCYBB Accession number M10277, verison M10277.1, GI:177967.

19. (New) The method of claim 16, characterised in that it uses a composition of universal primers that hybridise with one or more regions of the cytoplasmic beta-actin gene selected from the group consisting of the region between positions 1130 and 1473 of the cytoplasmic beta-actin gene, the region between positions 1452 and 2063 of the cytoplasmic beta-actin gene, the region between positions 2438 and 2680 of the cytoplasmic beta-actin gene, and the region between positions 2642 and 2960 of the cytoplasmic beta-actin gene, said position numbers being relative to SEQ ID NO:9 which comprises the full DNA sequence of the human locus HUMACCYBB Accession number M10277, verison M10277.1, GI:177967.